Listing of Claims

This listing of claims will replace all prior versions and listings of claims in this application.

1. [Currently Amended] Method for the preparation of a strain of evolved micro-organisms for the production of 1,2-propanediol by the metabolism of a simple carbon source, said ~~which~~ method comprising growing ~~comprises the growth~~ an initial bacterial strain, under selection pressure in an appropriate growth medium comprising ~~containing~~ a simple carbon source, said initial bacterial strain ~~that has undergone~~ comprising a deletion of the gene *tpiA* and ~~the~~ a deletion of at least one gene involved in the conversion of methylglyoxal (propanal) into lactate, in order to cause evolution ~~to evolve~~, in said initial strain, of one or more genes involved in the biosynthesis pathway from DHAP to methylglyoxal and then to 1,2-propanediol towards evolved genes having ~~that possess~~ an improved "1,2-propanediol synthase" activity, ~~which resulting~~ then selecting and isolating ~~evolved~~ strain or strains of evolved micro-organisms ~~that possess~~ having an improved "1,2-propanediol synthase" activity ~~are then selected and isolated~~.
2. [Currently Amended] ~~Method according to Claim 1, caracterised in that~~ The method of claim 1, wherein the gene involved in the conversion of methylglyoxal into lactate is selected from the group consisting in *gloA*, *aldA* and ~~or~~ a*ldB*.
3. [Currently Amended] ~~Method according to either of Claims 1 or 2, characterized in that~~ The method of claim 1, wherein the initial strain ~~has undergone the~~ comprises deletion of the genes *gloA, aldA,aldB* and *tpiA*.
4. [Currently Amended] ~~Method according to any of Claims 1 to 3, characterized in that~~ The method of claim 1, wherein the initial strain ~~has also undergone the~~ comprises deletion of the genes *IdhA, pflA, pflB, adhE* and *edd*.

5. [Currently Amended] ~~Method according to any of Claims to 4, characterized in that~~ The method of claim 1, wherein the initial strain also contains at least one gene coding for an enzyme that favours the metabolism of pyruvate to acetate.

6. [Currently Amended] ~~Method according to Claim 5, characterized in that~~ The method of claim 1, wherein the enzyme that favours the metabolism of pyruvate into acetate has low sensitivity to inhibition by NADH.

7. [Currently Amended] ~~Method according to either of Claims 5 or 6, characterized in that~~ The method of claim 5, wherein the said enzyme that favours the metabolism of pyruvate into acetate, favours the metabolism of pyruvate towards the production of acetyl-CoA and NADH.

8. [Currently Amended] ~~Method according to Claim 7, characterized in that~~ The method of claim 7, wherein the enzyme that favours the metabolism of pyruvate towards the production of acetyl-CoA and NADH is a pyruvate dehydrogenase complex.

9. [Currently Amended] ~~Method according to any of Claims 6 to 8, characterised in that~~ The method of claim 6, wherein the enzyme that favours the metabolism of pyruvate into acetate is an endogenous enzyme.

10. [Currently Amended] ~~Method according to any of Claims 1 to 9, characterised in~~ that The method of claim 1, wherein one or more heterologous genes coding for one or more enzymes involved in the conversion of acetyl-CoA and acetate into acetone are introduced into the evolved ~~strain~~ microorganisms.

11. [Currently Amended] ~~Method according to Claim 10, characterised in that~~ The method of claim 10, wherein one the heterologous gene or genes coding for one or more enzymes involved in the conversion of acetyl-CoA and acetate are from *C. acetobutylicum*.

12. [Currently Amended] ~~Method according to either of Claims 10 or 11, characterised in that~~ The method of claim 10, wherein ~~an evolved~~ the modified evolved strain comprising one or more heterologous genes coding for one or more enzymes involved in the conversion of acetyl-CoA and acetate into acetone ~~obtained according to either of Claims 10 or 11~~ is grown under selection pressure in an appropriate growth medium ~~containing~~ comprising a simple carbon source in order to cause, in said evolved modified evolved strain, the evolution of one or more genes involved in the conversion of acetyl-CoA and acetate to acetone towards an improved "acetone synthase" activity ~~The~~, the second generation of resulting evolved micro-organisms ~~that possess~~ having an improved "1,2-propanediol synthase" activity and an improved "acetone synthase" activity are then selected and isolated.

13. [Currently Amended] ~~Method according to any of the preceding claims, characterised in that~~ The method of claim 1, wherein the strain is selected from the group consisting of ~~a strain of~~ bacterium, a yeast and ~~or~~ a fungus.

14. [Currently Amended] ~~Method according to Claim 13, characterised in that~~ The method of claim 13, wherein the strain is selected from the group consisting of ~~a strain of~~ *Escherichia*~~, in particular E.coli,~~ and *Corynebacterium*~~, in particular C. glutamicum~~.

15. [Cancelled].

16. [Currently amended] Evolved strain that can be obtained by the method according to any of Claims 1 ~~to14~~.

17. [Original] Strain according to Claim 16, in which the gene *lpd* has a point mutation whereby alanine 55 is replaced by valine.

18. [Currently amended] Method of preparation of 1,2-propanediol ~~in which~~ wherein an evolved strain of claim 16 is grown ~~according to either of Claims 16 or 17~~ in an appropriate growth medium containing a simple carbon source, and wherein ~~in which~~ the 1,2-propanediol produced is recovered.

19. [Currently amended] ~~Method according to Claim 18, characterised in that~~ The method of claim 18, wherein 1,2-propanediol and acetone are recovered.

20. [Currently amended] ~~Method according to either of Claims 18 or19, characterised in that~~ The method of claim 18, wherein 1,2-propanediol and/or acetone are purified.

21. [New] The method of claim 14, wherein the strain is selected among the group consisting of *E. coli*, and *C. glutamicum*.

22. [New] Initial bacterial strain of a microorganism comprising a deletion of the gene *tpiA* and a deletion of at least one gene involved in the conversion of methylglyoxal (propanal) into lactate.

23. [New] The strain of claim 22, wherein the gene involved in the conversion of methylglyoxal into lactate is selected among the group consisting in *gloA, aldA* and *aldB*.

24. [New] The method of claim 22, wherein the initial strain comprises deletion of the genes *gloA, aldA, aldB* and *tpiA*.

25. [New] The strain of claim 22, wherein the initial strain comprises deletion of the genes *ldhA, pflA, pflB, adhE* and *edd*.

26. [New] The strain of claim 22, wherein the initial strain also contains at least one gene coding for an enzyme that favours the metabolism of pyruvate to acetate.

27. [New] The strain of claim 22, wherein the enzyme that favours the metabolism of pyruvate into acetate has low sensitivity to inhibition by NADH.

28. [New] The strain of claim 27, wherein the said enzyme that favours the metabolism of pyruvate into acetate, favours the metabolism of pyruvate towards the production of acetyl-CoA and NADH.

29. [New] The strain of claim 27, wherein the enzyme that favours the metabolism of pyruvate towards the production of acetyl-CoA and NADH is a pyruvate dehydrogenase complex.

30. [New] The strain of claim 22, selected from the group consisting of a bacterium, a yeast and a fungus.

31. [New] The strain of claim 30, selected from the group consisting of *Escherichia* and *Corynebacterium.*

32. [New] The strain of claim 16, comprising a deletion of the gene *tpiA* and a deletion of at least one gene involved in the conversion of methylglyoxal (propanal) into lactate, selected from the group consisting in *gloA, aldA* and *aldB.*

33. [New] The strain of claim 16, comprising deletion of the genes *gloA, aldA, aldB* and *tpiA.*

34. [New] The strain of claim 16, comprising deletion of the genes *IdhA, pflA, pflB, adhE* and *edd.*

35. [New] The strain of claim 16, comprising at least one gene coding for an enzyme that favours the metabolism of pyruvate to acetate.

36. [New] The strain of claim 36, wherein the enzyme that favours the metabolism of pyruvate into acetate has low sensitivity to inhibition by NADH.

37. [New] The strain of claim 36, wherein the said enzyme that favours the metabolism of pyruvate into acetate, favours the metabolism of pyruvate towards the production of acetyl-CoA and NADH.

38. [New] The strain of claim 37, wherein the enzyme that favours the metabolism of pyruvate towards the production of acetyl-CoA and NADH is a pyruvate dehydrogenase complex.

39. [[New] The strain of claim 36, wherein the enzyme that favours the metabolism of pyruvate into acetate is an endogenous enzyme.

40. [New] The strain of claim 16, comprising one or more heterologous genes coding for one or more enzymes involved in the conversion of acetyl-CoA and acetate into acetone.

41. [New] The strain of claim 40, wherein one the heterologous gene or genes coding for one or more enzymes involved in the conversion of acetyl-CoA and acetate is from *C. acetobutylicum.*

42. [New] The strain of claim 16, selected from the group consisting of a bacterium, a yeast and a fungus.

43. [New] The strain of claim 16, selected from the group consisting of *Escherichia,* and *Corynebacterium.*

44. [New] The strain of claim 17, selected from the group consisting of a bacterium, a yeast and a fungus.

45. [New] The strain of claim 17, selected from the group consisting of *Escherichia,* and *Corynebacterium.*

46. [New] Evolved strain that can be obtained by the method of Claim 10.

47. [New] The strain of Claim 46, in which the gene *Ipd* has a point mutation whereby alanine 55 is replaced by valine.

48. [New] The strain of claim 46, selected from the group consisting of a bacterium, a yeast and a fungus.

49. New] The strain of claim 46, selected from the group consisting of *Escherichia* and *Corynebacterium.*